

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: Adams, Camilia W.
 Ashkenazi, Avi J.
 Chuntharapai, Anan
 Kim, Kyung J.

10 (ii) TITLE OF INVENTION: Apo-2 Receptor

(iii) NUMBER OF SEQUENCES: 14

15 (iv) CORRESPONDENCE ADDRESS:
 (A) ADDRESSEE: Genentech, Inc.
 (B) STREET: 1 DNA Way
 (C) CITY: South San Francisco
 (D) STATE: California
 (E) COUNTRY: USA
 20 (F) ZIP: 94080

(v) COMPUTER READABLE FORM:
 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: WinPatin (Genentech)

25 (vi) CURRENT APPLICATION DATA:
 (A) APPLICATION NUMBER:
 (B) FILING DATE:
 (C) CLASSIFICATION:

30 (viii) ATTORNEY/AGENT INFORMATION:
 (A) NAME: Marschang, Diane L.
 (B) REGISTRATION NUMBER: 35,600
 (C) REFERENCE/DOCKET NUMBER: P1101R2

35 (ix) TELECOMMUNICATION INFORMATION:
 (A) TELEPHONE: 650/225-5416
 (B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 411 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

45 Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg
 1 5 10 15

50 Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro
 20 25 30

55 Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val
 35 40 45

60 Leu Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp
 50 55 60

Leu	Ala	Pro	Gln	Gln	Arg	Ala	Ala	Pro	Gln	Gln	Lys	Arg	Ser	Ser	
65														75	
5	Pro	Ser	Glu	Gly	Leu	Cys	Pro	Pro	Gly	His	His	Ile	Ser	Glu	Asp
					80					85					90
10	Gly	Arg	Asp	Cys	Ile	Ser	Cys	Lys	Tyr	Gly	Gln	Asp	Tyr	Ser	Thr
					95					100					105
15	His	Trp	Asn	Asp	Leu	Leu	Phe	Cys	Leu	Arg	Cys	Thr	Arg	Cys	Asp
					110					115					120
20	Ser	Gly	Glu	Val	Glu	Leu	Ser	Pro	Cys	Thr	Thr	Arg	Asn	Thr	
					125					130					135
25	Val	Cys	Gln	Cys	Glu	Glu	Gly	Thr	Phe	Arg	Glu	Glu	Asp	Ser	Pro
					140					145					150
30	Glu	Met	Cys	Arg	Lys	Cys	Arg	Thr	Gly	Cys	Pro	Arg	Gly	Met	Val
					155					160					165
35	Lys	Val	Gly	Asp	Cys	Thr	Pro	Trp	Ser	Asp	Ile	Glu	Cys	Val	His
					170					175					180
40	Lys	Glu	Ser	Gly	Ile	Ile	Ile	Gly	Val	Thr	Val	Ala	Ala	Val	Val
					185					190					195
45	Leu	Ile	Val	Ala	Val	Phe	Val	Cys	Lys	Ser	Leu	Leu	Trp	Lys	Lys
					200					205					210
50	Val	Leu	Pro	Tyr	Leu	Lys	Gly	Ile	Cys	Ser	Gly	Gly	Gly	Asp	
					215					220					225
55	Pro	Glu	Arg	Val	Asp	Arg	Ser	Ser	Gln	Arg	Pro	Gly	Ala	Glu	Asp
					230					235					240
60	Asn	Val	Leu	Asn	Glu	Ile	Val	Ser	Ile	Leu	Gln	Pro	Thr	Gln	Val
					245					250					255
65	Pro	Glu	Gln	Glu	Met	Glu	Val	Gln	Glu	Pro	Ala	Glu	Pro	Thr	Gly
					260					265					270
70	Val	Asn	Met	Leu	Ser	Pro	Gly	Glu	Ser	Glu	His	Leu	Leu	Glu	Pro
					275					280					285
75	Ala	Glu	Ala	Glu	Arg	Ser	Gln	Arg	Arg	Arg	Leu	Leu	Val	Pro	Ala
					290					295					300
80	Asn	Glu	Gly	Asp	Pro	Thr	Glu	Thr	Leu	Arg	Gln	Cys	Phe	Asp	Asp
					305					310					315
85	Phe	Ala	Asp	Leu	Val	Pro	Phe	Asp	Ser	Trp	Glu	Pro	Leu	Met	Arg
					320					325					330
90	Lys	Leu	Gly	Leu	Met	Asp	Asn	Glu	Ile	Lys	Val	Ala	Lys	Ala	Glu
					335					340					345
95	Ala	Ala	Gly	His	Arg	Asp	Thr	Leu	Tyr	Thr	Met	Leu	Ile	Lys	Trp
					350					355					360

Val	Asn	Lys	Thr	Gly	Arg	Asp	Ala	Ser	Val	His	Thr	Leu	Leu	Asp	
														365	
														370	
														375	
5	Ala	Leu	Glu	Thr	Leu	Gly	Glu	Arg	Leu	Ala	Lys	Gln	Lys	Ile	Glu
															380
														385	
														390	
	Asp	His	Leu	Leu	Ser	Ser	Gly	Lys	Phe	Met	Tyr	Leu	Glu	Gly	Asn
															395
10															400
															405
	Ala	Asp	Ser	Ala	Xaa	Ser									
															410 411

(2) INFORMATION FOR SEQ ID NO:2:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1799 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

25	CCACACGCGTC	CGCATAAAATC	AGCACCGGGC	CGGAGAACCC	CGCAATCTCT	50
	GCGCCCACAA	AATACACCGA	CGATGCCCGA	TCTACTTTAA	GGGCTGAAAC	100
30	CCACGGGCCT	GAGAGACTAT	AAGAGCGTTC	CCTACCGCC	ATG GAA	145
					Met Glu	
					1	
35	CAA CGG GGA CAG AAC GCC CCG GCT TCG GGG GCC CGG	184				
	Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg					
	5	10	15			
40	AAA AGG CAC GGC CCA GGA CCC AGG GAG GCG CGG GGA GCC	223				
	Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala					
	20	25				
45	AGG CCT GGG CTC CGG GTC CCC AAG ACC CTT GTG CTC GTT	262				
	Arg Pro Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val					
	30	35	40			
50	GTC GCC GCG GTC CTG CTG TTG GTC TCA GCT GAG TCT GCT	301				
	Val Ala Ala Val Leu Leu Leu Val Ser Ala Glu Ser Ala					
	45	50				
55	CTG ATC ACC CAA CAA GAC CTA GCT CCC CAG CAG AGA GCG	340				
	Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln Gln Arg Ala					
	55	60	65			
	GCC CCA CAA CAA AAG AGG TCC AGC CCC TCA GAG GGA TTG	379				
	Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu					
	70	75	80			
	TGT CCA CCT GGA CAC CAT ATC TCA GAA GAC GGT AGA GAT	418				
	Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp					
	85	90				

5	TGC ATC TCC TGC AAA TAT GGA CAG GAC TAT AGC ACT CAC 457		
	Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His		
	95	100	105
10	TGG AAT GAC CTC CTT TTC TGC TTG CGC TGC ACC AGG TGT 496		
	Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys		
	110	115	
15	GAT TCA GGT GAA GTG GAG CTA AGT CCC TGC ACC ACG ACC 535		
	Asp Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr Thr		
	120	125	130
20	AGA AAC ACA GTG TGT CAG TGC GAA GAA GGC ACC TTC CGG 574		
	Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe Arg		
	135	140	145
25	GAA GAA GAT TCT CCT GAG ATG TGC CGG AAG TGC CGC ACA 613		
	Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr		
	150	155	
30	GGG TGT CCC AGA GGG ATG GTC AAG GTC GGT GAT TGT ACA 652		
	Gly Cys Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr		
	160	165	170
35	CCC TGG AGT GAC ATC GAA TGT GTC CAC AAA GAA TCA GGC 691		
	Pro Trp Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly		
	175	180	
40	ATC ATC ATA GGA GTC ACA GTT GCA GCC GTA GTC TTG ATT 730		
	Ile Ile Ile Gly Val Thr Val Ala Ala Val Val Leu Ile		
	185	190	195
45	GTG GCT GTG TTT GTT TGC AAG TCT TTA CTG TGG AAG AAA 769		
	Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys		
	200	205	210
50	GTC CTT CCT TAC CTG AAA GGC ATC TGC TCA GGT GGT GGT 808		
	Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly		
	215	220	
55	GGG GAC CCT GAG CGT GTG GAC AGA AGC TCA CAA CGA CCT 847		
	Gly Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro		
	225	230	235
60	GGG GCT GAG GAC AAT GTC CTC AAT GAG ATC GTG AGT ATC 886		
	Gly Ala Glu Asp Asn Val Leu Asn Glu Ile Val Ser Ile		
	240	245	
65	TTG CAG CCC ACC CAG GTC CCT GAG CAG GAA ATG GAA GTC 925		
	Leu Gln Pro Thr Gln Val Pro Glu Gln Glu Met Glu Val		
	250	255	260
70	CAG GAG CCA GCA GAG CCA ACA GGT GTC AAC ATG TTG TCC 964		
	Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Met Leu Ser		
	265	270	275
75	CCC GGG GAG TCA GAG CAT CTG CTG GAA CCG GCA GAA GCT 1003		
	Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala		
	280	285	

GAA AGG TCT CAG AGG AGG CTG CTG GTT CCA GCA AAT 1042
 Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn
 290 295 300
 5 GAA GGT GAT CCC ACT GAG ACT CTG AGA CAG TGC TTC GAT 1081
 Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp
 305 310
 10 GAC TTT GCA GAC TTG GTG CCC TTT GAC TCC TGG GAG CCG 1120
 Asp Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro
 315 320 325
 15 CTC ATG AGG AAG TTG GGC CTC ATG GAC AAT GAG ATA AAG 1159
 Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile Lys
 330 335 340
 GTG GCT AAA GCT GAG GCA GCG GGC CAC AGG GAC ACC TTG 1198
 Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu
 345 350
 20 TAC ACG ATG CTG ATA AAG TGG GTC AAC AAA ACC GGG CGA 1237
 Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg
 355 360 365
 25 GAT GCC TCT GTC CAC ACC CTG CTG GAT GCC TTG GAG ACG 1276
 Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr
 370 375
 30 CTG GGA GAG AGA CTT GCC AAG CAG AAG ATT GAG GAC CAC 1315
 Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His
 380 385 390
 35 TTG TTG AGC TCT GGA AAG TTC ATG TAT CTA GAA GGT AAT 1354
 Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
 395 400 405
 40 GCA GAC TCT GCC WTG TCC TAAGTGTG ATTCTCTTCA GGAAGTGAGA 1400
 Ala Asp Ser Ala Xaa Ser
 410 411
 CCTTCCCTGG TTTACCTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC 1450
 AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC 1500
 45 CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAACCTT TTCACTGCAC 1550
 TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAAT 1600
 GTCTGGATCA TTCCGTTGT GCGTACTTTG AGATTTGGTT TGGGATGTCA 1650
 50 TTGTTTCAC AGCACCTTT TATCCTAATG TAAATGCTTT ATTTATTTAT 1700
 TTGGGCTACA TTGTAAGATC CATCTACAAA AAAAAAAA AAAAAAAAG 1750
 55 GGCGGCCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC 1799

(2) INFORMATION FOR SEQ ID NO:3:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs
 (B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGAGCCGCT CATGAGGAAG TTGGGCCTCA TGGACAATGA GATAAAGGTG 50
 GCTAAAGCTG AGGCAGCGGG 70

10 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

25 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

35 AGGATGGGAA GTGTGTGATA TATCCTTGAT 30

40 (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 930 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATG ACC ATG ATT ACG CCA AGC TTT GGA GCC TTT TTT 36
 Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe
 50 1 5 10

55 TTG GAG ATT TTC AAC GTG AAA AAA TTA TTA TTC GCA ATT 75
 Leu Glu Ile Phe Asn Val Lys Lys Leu Leu Phe Ala Ile
 15 20 25

CCT TTA GTT GTT CCT TTC TAT GCG GCC CAG CCG GCC ATG 114
 Pro Leu Val Val Pro Phe Tyr Ala Ala Gln Pro Ala Met
 30 35

	GCC GAG GTG CAG CTG GTG CAG TCT GGG GGA GGT GTG GAA	153
	Ala Glu Val Gln Leu Val Gln Ser Gly Gly Gly Val Glu	
	40 45 50	
5	CGG CCG GGG GGG TCC CTG AGA CTC TCC TGT GCA GCC TCT	192
	Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser	
	55 60	
10	GGA TTC ACC TTT GAT GAT TAT GGC ATG AGC TGG GTC CGC	231
	Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg	
	65 70 75	
15	CAA GCT CCA GGG AAG GGG CTG GAG TGG GTC TCT GGT ATT	270
	Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile	
	80 85 90	
	AAT TGG AAT GGT GGT AGC ACA GGA TAT GCA GAC TCT GTG	309
	Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val	
	95 100	
20	AAG GGC CGA GTC ACC ATC TCC AGA GAC AAC GCC AAG AAC	348
	Lys Gly Arg Val Thr Ile Ser Arg Asp Asn Ala Lys Asn	
	105 110 115	
25	TCC CTG TAT CTG CAA ATG AAC AGC CTG AGA GCC GAG GAC	387
	Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp	
	120 125	
30	ACG GCC GTA TAT TAC TGT GCG AAA ATC CTG GGT GCC GGA	426
	Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala Gly	
	130 135 140	
35	CGG GGC TGG TAC TTC GAT CTC TGG GGG AAG GGG ACC ACG	465
	Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr	
	145 150 155	
40	GTC ACC GTC TCG AGT GGT GGA GGC GGT TCA GGC GGA GGT	504
	Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly	
	160 165	
	GGC AGC GGC GGT GGC GGA TCG TCT GAG CTG ACT CAG GAC	543
	Gly Ser Gly Gly Ser Ser Glu Leu Thr Gln Asp	
	170 175 180	
45	CCT GCT GTG TCT GTG GCC TTG GGA CAG ACA GTC AGG ATC	582
	Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile	
	185 190	
50	ACA TGC CAA GGA GAC AGC CTC AGA AGC TAT TAT GCA AGC	621
	Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser	
	195 200 205	
55	TGG TAC CAG CAG AAG CCA GGA CAG GCC CCT GTA CTT GTC	660
	Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val	
	210 215 220	
60	ATC TAT GGT AAA AAC AAC CGG CCC TCA GGG ATC CCA GAC	699
	Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp	
	225 230	

CGA TTC TCT GGC TCC AGC TCA GGA AAC ACA GCT TCC TTG 738
 Arg Phe Ser Gly Ser Ser Gly Asn Thr Ala Ser Leu
 235 240 245

5 ACC ATC ACT GGG GCT CAG GCG GAA GAT GAG GCT GAC TAT 777
 Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr
 250 255

10 TAC TGT AAC TCC CGG GAC AGC AGT GGT AAC CAT GTG GTA 816
 Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val Val
 260 265 270

15 TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA GGT GCG GCC 855
 Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Ala Ala
 275 280 285

GCA CAT CAT CAT CAC CAT CAC GGG GCC GCA GAA CAA AAA 894
 Ala His His His His His Gly Ala Ala Glu Gln Lys
 290 295

20 CTC ATC TCA GAA GAG GAT CTG AAT GGG GCC GCA TAG 930
 Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala
 300 305 309

25 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 939 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

35 ATG ACC ATG ATT ACG CCA AGC TTT GGA GCC TTT TTT 36
 Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe
 1 5 10

40 TTG GAG ATT TTC AAC GTG AAA AAA TTA TTA TTC GCA ATT 75
 Leu Glu Ile Phe Asn Val Lys Lys Leu Leu Phe Ala Ile
 15 20 25

45 CCT TTA GTT GTT CCT TTC TAT GCG GCC CAG CCG GCC ATG 114
 Pro Leu Val Val Pro Phe Tyr Ala Ala Gln Pro Ala Met
 30 35

50 GCC GGG GTG CAG CTG GTG GAG TCT GGG GGA GGC TTG GTC 153
 Ala Gly Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
 40 45 50

55 CAG CCT GGG GGG TCC CTG AGA CTC TCC TGT GCA GCC TCT 192
 Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
 55 60

55 GGA TTC ACC TTT AGT AGC TAT TGG ATG AGC TGG GTC CGC 231
 Gly Phe Thr Phe Ser Ser Tyr Trp Met Ser Trp Val Arg
 65 70 75

10	CAG GCT CCA GGG AAG GGG CTG GAG TGG GTG GCC AAC ATA 270
	Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Asn Ile
	80 85 90
5	AAG CAA GAT GGA AGT GAG AAA TAC TAT GTG GAC TCT GTG 309
	Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
	95 100
10	AAG GGC CGA TTC ACC ATC TCC AGA GAC AAC GCC AAG AAC 348
	Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
	105 110 115
15	TCA CTG TAT CTG CAA ATG AAC AGC CTG AGA GCC GAG GAC 387
	Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
	120 125
20	ACG GCT GTG TAT TAC TGT GCG AGA GAT CTT TTA AAG GTC 426
	Thr Ala Val Tyr Tyr Cys Ala Arg Asp Leu Leu Lys Val
	130 135 140
25	AAG GGC AGC TCG TCT GGG TGG TTC GAC CCC TGG GGG AGA 465
	Lys Gly Ser Ser Gly Trp Phe Asp Pro Trp Gly Arg
	145 150 155
30	GGG ACC ACG GTC ACC GTC TCG AGT GGT GGA GGC GGT TCA 504
	Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser
	160 165
35	GGC GGA GGT GGT AGC GGC GGT GGC GGA TCG TCT GAG CTG 543
	Gly Gly Gly Ser Gly Gly Gly Ser Ser Glu Leu
	170 175 180
40	ACT CAG GAC CCT GCT GTG TCT GTG GCC TTG GGA CAG ACA 582
	Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr
	185 190
45	GTC AGG ATC ACA TGC CAA GGA GAC AGC CTC AGA AGC TAT 621
	Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr
	195 200 205
50	TAT GCA AGC TGG TAC CAG CAG AAG CCA GGA CAG GCC CCT 660
	Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
	210 215 220
55	GTA CTT GTC ATC TAT GGT AAA AAC AAC CGG CCC TCA GGG 699
	Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly
	225 230
60	ATC CCA GAC CGA TTC TCT GGC TCC AGC TCA GGA AAC ACA 738
	Ile Pro Asp Arg Phe Ser Gly Ser Ser Gly Asn Thr
	235 240 245
65	GCT TCC TTG ACC ATC ACT GGG GCT CAG GCG GAA GAT GAG 777
	Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu
	250 255
70	GCT GAC TAT TAC TGT AAC TCC CGG GAC AGC AGT GGT AAC 816
	Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn
	260 265 270

CAT GTG GTA TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA 855
 His Val Val Phe Gly Gly Thr Lys Leu Thr Val Leu
 275 280 285
 5 GGT GCG GCC GCA CAT CAT CAT CAC CAC GGG GCC GCA 894
 Gly Ala Ala Ala His His His His His Gly Ala Ala
 290 295
 10 GAA CAA AAA CTC ATC TCA GAA GAG GAT CTG AAT GGG GCC 933
 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala
 300 305 310
 15 GCA TAG 939
 Ala
 312

(2) INFORMATION FOR SEQ ID NO:8:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 933 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATG ACC ATG ATT ACG CCA AGC TTT GGA GCC TTT TTT 36
 Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe
 30 1 5 10

TTG GAG ATT TTC AAC GTG AAA AAA TTA TTA TTC GCA ATT 75
 Leu Glu Ile Phe Asn Val Lys Lys Leu Leu Phe Ala Ile
 35 15 20 25

CCT TTA GTT GTT CCT TTC TAT GCG GCC CAG CCG GCC ATG 114
 Pro Leu Val Val Pro Phe Tyr Ala Ala Gln Pro Ala Met
 30 35

40 GCC CAG GTG CAG CTG GTG CAG TCT GGG GGA GGC GTG GTC 153
 Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val
 40 45 50

45 CAG CCT GGG CGG TCC CTG AGA CTC TCC TGT GCA GCT TCT 192
 Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser
 55 60

GGG TTC ATT TTC AGT AGT TAT GGG ATG CAC TGG GTC CGC 231
 Gly Phe Ile Phe Ser Ser Tyr Gly Met His Trp Val Arg
 50 65 70 75

CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG GCA GGT ATT 270
 Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Gly Ile
 80 85 90

55 TTT TAT GAT GGA GGT AAT AAA TAC TAT GCA GAC TCC GTG 309
 Phe Tyr Asp Gly Gly Asn Lys Tyr Tyr Ala Asp Ser Val
 95 100

	AAG	GGC	CGA	TTC	ACC	ATC	TCC	AGA	GAC	AAT	TCC	AAG	AAC	348
	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	
	105				110						115			
5	ACG	CTG	TAT	CTG	CAA	ATG	AAC	AGC	CTG	AGA	GCT	GAG	GAC	387
	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	
	120				125									
10	ACG	GCT	GTG	TAT	TAC	TGT	GCG	AGA	GAT	AGG	GGC	TAC	TAC	426
	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Asp	Arg	Gly	Tyr	Tyr	
	130				135						140			
15	TAC	ATG	GAC	GTC	TGG	GGC	AAA	GGG	ACC	ACG	GTC	ACC	GTC	465
	Tyr	Met	Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val	Thr	Val	
	145				150						155			
20	TCC	TCA	GGT	GGA	GGC	GGT	TCA	GGC	GGA	GGT	GGC	TCT	GGC	504
	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	
	160				165									
25	GGT	GGC	GGA	TCG	CAG	TCT	GTG	TTG	ACG	CAG	CCG	CCC	TCA	543
	Gly	Gly	Gly	Ser	Gln	Ser	Val	Leu	Thr	Gln	Pro	Pro	Ser	
	170				175						180			
30	GTG	TCT	GGG	GCC	CCA	GGA	CAG	AGG	GTC	ACC	ATC	TCC	TGC	582
	Val	Ser	Gly	Ala	Pro	Gly	Gln	Arg	Val	Thr	Ile	Ser	Cys	
	185				190									
35	ACT	GGG	AGA	AGC	TCC	AAC	ATC	GGG	GCA	GGT	CAT	GAT	GTA	621
	Thr	Gly	Arg	Ser	Ser	Asn	Ile	Gly	Ala	Gly	His	Asp	Val	
	195				200						205			
40	CAC	TGG	TAC	CAG	CAA	CTT	CCA	GGA	ACA	GCC	CCC	AAA	CTC	660
	His	Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Thr	Ala	Pro	Lys	Leu	
	210				215						220			
45	CTC	ATC	TAT	GAT	GAC	AAT	CGG	CCC	TCA	GGG	GTC	CCT	699	
	Leu	Ile	Tyr	Asp	Asp	Ser	Asn	Arg	Pro	Ser	Gly	Val	Pro	
	225				230									
50	GAC	CGA	TTC	TCT	GGC	TCC	AGG	TCT	GGC	ACC	TCA	GCC	TCC	738
	Asp	Arg	Phe	Ser	Gly	Ser	Arg	Ser	Gly	Thr	Ser	Ala	Ser	
	235				240						245			
55	CTG	GCC	ATC	ACT	GGG	CTC	CAG	GCT	GAA	GAT	GAG	GCT	GAT	777
	Leu	Ala	Ile	Thr	Gly	Leu	Gln	Ala	Glu	Asp	Glu	Ala	Asp	
	250				255									
60	TAT	TAC	TGC	CAG	TCC	TAT	GAC	AGC	AGC	CTG	AGG	GGT	TCG	816
	Tyr	Tyr	Cys	Gln	Ser	Tyr	Asp	Ser	Ser	Leu	Arg	Gly	Ser	
	260				265						270			
65	GTA	TTC	GGC	GGA	GGG	ACC	AAG	GTC	ACT	GTC	CTA	GGT	GCG	855
	Val	Phe	Gly	Gly	Gly	Thr	Lys	Val	Thr	Val	Leu	Gly	Ala	
	275				280						285			
70	GCC	GCA	CAT	CAT	CAT	CAC	CAT	CAC	GGG	GCC	GCA	GAA	CAA	894
	Ala	Ala	His	His	His	His	His	His	Gly	Ala	Ala	Glu	Gln	
	290				295									

AAA CTC ATC TCA GAA GAG GAT CTG AAT GGG GCC GCA 930
 Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala
 300 305 310

5 TAG 933

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 309 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

15 Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile
 1 5 10 15

20 Phe Asn Val Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro
 20 25 30

25 Phe Tyr Ala Ala Gln Pro Ala Met Ala Glu Val Gln Leu Val Gln
 35 40 45

30 Ser Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser
 50 55 60

35 Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp
 65 70 75

40 Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile
 80 85 90

45 Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
 95 100 105

50 Arg Val Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 110 115 120

55 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 125 130 135

60 Ala Lys Ile Leu Gly Ala Gly Arg Gly Trp Tyr Phe Asp Leu Trp
 140 145 150

65 Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser
 155 160 165

70 Gly Gly Gly Ser Gly Gly Gly Ser Ser Glu Leu Thr Gln
 170 175 180

75 Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr
 185 190 195

80 Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln
 200 205 210

85 Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn
 215 220 225

60

	Asn	Arg	Pro	Ser	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Ser	Ser
						230					235				
															240
	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Thr	Gly	Ala	Gln	Ala	Glu	Asp
5															
											245		250		255
	Glu	Ala	Asp	Tyr	Tyr	Cys	Asn	Ser	Arg	Asp	Ser	Ser	Gly	Asn	His
											260		265		270
10	Val	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	Ala	Ala
											275		280		285
	Ala	His	His	His	His	His	His	Gly	Ala	Ala	Glu	Gln	Lys	Leu	Ile
											290		295		300
15															
	Ser	Glu	Glu	Asp	Leu	Asn	Gly	Ala	Ala						
											305		309		

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Thr	Met	Ile	Thr	Pro	Ser	Phe	Gly	Ala	Phe	Phe	Leu	Glu	Ile
1				5						10			15	
Phe	Asn	Val	Lys	Lys	Leu	Leu	Phe	Ala	Ile	Pro	Leu	Val	Val	Pro
				20						25			30	
Phe	Tyr	Ala	Ala	Gln	Pro	Ala	Met	Ala	Gly	Val	Gln	Leu	Val	Glut
				35					40			45		
Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser
				50					55			60		
Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Trp	Met	Ser	Trp
				65					70			75		
Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Asn	Ile
				80					85			90		
Lys	Gln	Asp	Gly	Ser	Glu	Lys	Tyr	Tyr	Val	Asp	Ser	Val	Lys	Gly
				95					100			105		
Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr	Leu
				110					115			120		
Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				125					130			135		
Ala	Arg	Asp	Leu	Leu	Lys	Val	Lys	Gly	Ser	Ser	Ser	Gly	Trp	Phe
				140					145			150		
Asp	Pro	Trp	Gly	Arg	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly
				155					160			165		

	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Ser	Glu	
				170			175							180	
5	Leu	Thr	Gln	Asp	Pro	Ala	Val	Ser	Val	Ala	Leu	Gly	Gln	Thr	Val
				185			190							195	
	Arg	Ile	Thr	Cys	Gln	Gly	Asp	Ser	Leu	Arg	Ser	Tyr	Tyr	Ala	Ser
				200			205							210	
10	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Val	Leu	Val	Ile	Tyr
				215			220							225	
	Gly	Lys	Asn	Asn	Arg	Pro	Ser	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly
15				230			235							240	
	Ser	Ser	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Thr	Gly	Ala	Gln
				245			250							255	
20	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Asn	Ser	Arg	Asp	Ser	Ser
				260			265							270	
	Gly	Asn	His	Val	Val	Phe	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	
				275			280							285	
25	Gly	Ala	Ala	Ala	His	His	His	His	His	Gly	Ala	Ala	Glu	Gln	
				290			295							300	
	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Asn	Gly	Ala	Ala			
30				305			310								

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 310 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

40	Met	Thr	Met	Ile	Thr	Pro	Ser	Phe	Gly	Ala	Phe	Phe	Leu	Glu	Ile
	1			5				10						15	
	Phe	Asn	Val	Lys	Lys	Leu	Leu	Phe	Ala	Ile	Pro	Leu	Val	Val	Pro
45				20				25						30	
	Phe	Tyr	Ala	Ala	Gln	Pro	Ala	Met	Ala	Gln	Val	Gln	Leu	Val	Gln
				35				40						45	
50	Ser	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser	
				50				55						60	
	Cys	Ala	Ala	Ser	Gly	Phe	Ile	Phe	Ser	Ser	Tyr	Gly	Met	His	Trp
				65				70						75	
55	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Gly	Ile
				80				85						90	
	Phe	Tyr	Asp	Gly	Gly	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly
				95				100						105	

Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	Leu	
														110	
														115	
														120	
5	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
															125
														130	
														135	
10	Ala	Arg	Asp	Arg	Gly	Tyr	Tyr	Tyr	Met	Asp	Val	Trp	Gly	Lys	Gly
															140
														145	
														150	
15	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly
															155
														160	
														165	
20	Gly	Ser	Gly	Gly	Gly	Ser	Gln	Ser	Val	Leu	Thr	Gln	Pro	Pro	
															170
														175	
														180	
25	Ser	Val	Ser	Gly	Ala	Pro	Gly	Gln	Arg	Val	Thr	Ile	Ser	Cys	Thr
															185
														190	
														195	
30	Gly	Arg	Ser	Ser	Asn	Ile	Gly	Ala	Gly	His	Asp	Val	His	Trp	Tyr
															200
														205	
														210	
35	Gln	Gln	Leu	Pro	Gly	Thr	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Asp	Asp
															215
														220	
														225	
40	Ser	Asn	Arg	Pro	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Arg
															230
														235	
														240	
45	Ser	Gly	Thr	Ser	Ala	Ser	Leu	Ala	Ile	Thr	Gly	Leu	Gln	Ala	Glu
															245
														250	
														255	
50	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Ser	Tyr	Asp	Ser	Ser	Leu	Arg
															260
														265	
														270	
55	Gly	Ser	Val	Phe	Gly	Gly	Gly	Thr	Lys	Val	Thr	Val	Leu	Gly	Ala
															275
														280	
														285	
60	Ala	Ala	His	His	His	His	His	Gly	Ala	Ala	Glu	Gln	Lys	Leu	
															290
														295	
														300	
65	Ile	Ser	Glu	Glu	Asp	Leu	Asn	Gly	Ala	Ala					
															305
														310	

(2) INFORMATION FOR SEQ ID NO:12:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

55 AGCGGATAAC AATTCACAC AGG 23

(2) INFORMATION FOR SEQ ID NO:13:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTCGTCTTTC CAGACGGTAG T 21

10 (2) INFORMATION FOR SEQ ID NO:14:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Ala Asp Pro Asn Arg Phe Arg Gly Lys Asp Leu
1 5 10 12

20